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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 10:47:40 : Search time 202.3 Seconds
(without alignments)
2866.003 Million cell updates/sec

Title: US-09-602-833a-3
Perfect score: 681
Sequence: 1 atggaattcgcgatactgc.....ctttagcctcaacttga 681

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 930621 seqs, 428662619 residues
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N.Geneseq..1101.*
2: /SID2/gcgdata/geneseq/geneseqn/NA1980.DAT.*
3: /SID2/gcgdata/geneseq/geneseqn/NA1981.DAT.*
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18: /SID2/gcgdata/geneseq/geneseqn/NA1996.DAT.*
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21: /SID2/gcgdata/geneseq/geneseqn/NA1999.DAT.*
22: /SID2/gcgdata/geneseq/geneseqn/NA2000.DAT.*
23: /SID2/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	681	100.0	681	22	AAF24903	Nucleotide sequence
2	681	100.0	1116	22	AAF24902	Nucleotide sequence
3	130.4	19.1	2056	22	AAH17218	Human CDNA sequence
4	78.6	11.5	936	22	AAF58252	Oligonucleotide D1
5	78.6	11.5	936	22	AAF58254	Oligonucleotide D1
6	78.6	11.5	936	22	AAF58257	Oligonucleotide D1
7	78.6	11.5	936	22	AAF58259	Oligonucleotide D2
8	78.6	11.5	936	22	AAF58262	Oligonucleotide D2
9	78.6	11.5	936	22	AAF58255	Oligonucleotide D1
10	77.4	11.4	936	22	AAF58252	Oligonucleotide D1
11	77.4	11.4	936	22	AAF58254	Oligonucleotide D1

c 12	77.4	11.4	936	22	AAF58257	Oligonucleotide D1
c 13	77.4	11.4	936	22	AAF58259	Oligonucleotide D2
c 14	77.4	11.4	936	22	AAF58262	Oligonucleotide D2
c 15	77.4	11.4	938	22	AAF58255	Oligonucleotide D1
16	57.4	8.4	1600	22	AA161075	Human polynucleot
17	57.4	8.4	1947	20	AA52247	Protein PRO239 CDN
18	57.4	8.4	1947	22	AA52247	Human PRO239 CDNA..
19	57.4	8.4	2384	19	AA30919	Human secreted pro
20	57.4	8.4	2384	22	AA598398	Human CDNA clone A
21	57.4	8.4	2412	22	AA159289	Human polynucleot
22	57.4	8.4	2641	21	AA52427	HTM clone 2709055
23	56.8	8.3	6242	21	AA599495	Human CDNA encodin
24	55.8	8.2	2410	22	AAH14179	Human CDNA sequenc
25	55.2	8.1	3159	21	AA599494	Human DNA encoding
26	55.2	8.1	3400	21	AA576598	Human ORF ORF2153
27	55.2	8.1	6125	22	AAH72745	Human cervical can
28	52.6	7.7	3138	21	AA30202	Human RING finger
29	51.8	7.6	2169	21	AA30203	Human RING finger
30	51	7.5	1986	22	AA526548	DNA encoding human
31	51	7.5	6470	22	AA158376	Human polynucleot
32	50.4	7.4	2620	22	AAH14529	Human CDNA sequenc
33	50.4	7.4	2840	22	AAH24250	Human Ras-binding
34	50.4	7.4	2847	22	AAH17735	Human CDNA sequenc
35	49.8	7.3	2694	21	AA45671	Nucleotide sequenc
36	48.6	7.1	5199	22	AA158164	Human polynucleot
37	47.6	7.0	2527	22	AA15457	Human CDNA sequenc
38	46.2	6.8	3675	21	AA521797	Human breast and o
39	43.4	6.4	861	22	AAH06813	Human CDNA clone (
40	42.8	6.3	6703	19	AA49536	Adenylate cyclase
41	42.4	6.2	502	21	AA500229	Human secreted pro
42	41.8	6.1	1710	22	AAH33095	Human colon cancer
43	40.6	6.0	1273	22	AAH34612	Human colon cancer
44	39.8	5.8	1470	21	AA578035	Human cancer assoc
45	39.8	5.8	3331	22	AA522442	Human CDNA encodin

ALIGNMENTS

RESULT 1	
ID AAF24903	standard; CDNA; 681 BP.
XX	
AC AAF24903;	
XX	
DT 20-APR-2001	(first entry)
XX	
DE	Nucleotide sequence of a human SGT4-2 polypeptide.
XX	
KW Human; SGT4; signal transduction; guanosine triphosphate binding protein;	
KW GTP binding protein; cancer; immune response; nutritional source;	
KW animal feed; ss.	
XX	
OS Homo sapiens.	
XX	
FH	Key
FT CDS.	1. 681
FT	/*tag= a
FT	/product= "SGT4"
PN	
PD WO200078959-A1.	
XX	
PD 28-DEC-2000.	
XX	
PF 22-JUN-2000; 2000WO-US17248.	
XX	
PR 23-JUN-1999; 99US-0140627.	
XX	
PA (LEXI-) LEXICON GENETICS INC.	
XX	
PI Turner AC, Zambrowicz B, Nehls M, Friedrich GA, Sands AT;	
XX	
DR WPI; 2001-032329/04.	

DR P-PSDB; AAB31564.
 XX New SGT4 genes and proteins, useful for diagnosing and treating
 PT disorders involving inappropriate regulation of a signal transduction
 PT mechanism e.g. cancer -
 XX
 PS Claim 1; Fig 3; 82pp; English.
 XX
 CC The present sequence encodes a human SGT4 polypeptide. SGT4 polypeptides
 CC are involved in signal transduction pathways regulated by guanosine
 CC triphosphate (GTP) binding proteins). SGT4 polynucleotides and
 CC polypeptides are for diagnosing and treating conditions related to a
 CC signal transduction mechanism involving SGT4 such as cancer. In
 CC addition, it can be used to detect the expression of SGT4 as markers of
 CC specific cells and tissues such as neuronal tissue, heart, liver,
 CC pancreas and adrenal gland. They are also useful for the construction of
 CC transgenic and knockout animals for studying SGT4 function in vivo and
 CC for the screening of SGT4 (ant)agonists in an animal model. Other more
 CC general uses include: as molecular weight markers on Southern gels; as
 CC chromosome markers or tags; as probes; for selecting and making
 CC oligomers for attachment to a gene chip; to raise anti-protein or
 CC anti-DNA antibodies or to elicit immune response. They are also
 CC also be used as nutritional sources or supplements such as in animal
 CC feed.
 XX
 SQ Sequence 681 BP; 212 A; 138 C; 142 G; 189 T; 0 other;

Query Match 100.0%; Score 681; DB 22; Length 681;
 Best Local Similarity 100.0%; Pred. No. 7.5e-198;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 atgagaattctgagatctgcaaaaaaaccaatctcaatcttcagcagaatcggtgt 60
 QY 61 ttgagaacctgaagaactcaatggtgttcacatactcgaagagatccctccgaa 120
 DB 61 ttgagaacctgaagaactcaatggtgttcacatactcgaagagatccctccgaa 120
 QY 121 ttggaagatttgaaaactcagagagactgagctgttcctggaactcgaattatgag 180
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 QY 121 ttggagatgttgaaaactcagagagactgagctgttcctggaactcgaattatgag 180
 DB 121 ttggagatgttgaaaactcagagagactgagctgttcctggaactcgaattatgag 180
 QY 181 ctgccttgaatgaatgaatctgaagaagttacattgttagatctcagcaaacaa 240
 DB 181 ctgccttgaatgaatgaatctgaagaagttacattgttagatctcagcaaacaa 240
 QY 241 ttctcagtgctccaactgtgtctcgtgagatgcaattgcaagtgttgatatacgc 300
 DB 241 ttctcagtgctccaactgtgtctcgtgagatgcaattgcaagtgttgatatacgc 300
 QY 301 agcaataactgaccgacactgcgcgaagatalagacaggtcagagagctcagagctt 360
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 DB 541 gatggcaatgaataatgaaagtgaacggatgcgcaacatttgaataaagaagtatg 600
 QY 601 aaagccatattggaagccttaagaagaagaatctgttccagctataccacaagaagt 660

DB 601 aaagccatattggaagccttaagaagaagaatctgttccagctataccacaagaagt 660
 QY 661 tctttagacctcaacttga 681
 DB 661 tctttagacctcaacttga 681

RESULT 2
 AAF24902
 ID AAF24902 standard; CDNA; 1116 BP.
 XX
 AC AAF24902;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of a human SGT4-1 polypeptide.
 XX
 KW Human; SGT4; signal transduction; guanosine triphosphate binding protein;
 KW GTP binding protein; cancer; immune response; nutritional source;
 KW animal feed; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..1116
 FT CDS /*tag= a
 FT /product= "SGT4"
 XX
 PN W0200078959-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 22-JUN-2000; 2000MO-US17248.
 XX
 PR 23-JUN-1999; 99US-0140627.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Turner AC, Zambrowicz B, Nehls M, Friedrich GA, Sands AT;
 XX
 DR WPI: 2001-032329/04.
 DR P-PSDB; AAB31563.
 XX
 XX New SGT4 genes and proteins, useful for diagnosing and treating
 PT disorders involving inappropriate regulation of a signal transduction
 PT mechanism e.g. cancer -
 XX
 PS Claim 1; Fig 1; 82pp; English.
 XX
 CC The present sequence encodes a human SGT4 polypeptide. SGT4 polypeptides
 CC are involved in signal transduction pathways regulated by guanosine
 CC triphosphate (GTP) binding proteins). SGT4 polynucleotides and
 CC polypeptides are for diagnosing and treating conditions related to a
 CC signal transduction mechanism involving SGT4 such as cancer. In
 CC addition, it can be used to detect the expression of SGT4 as markers of
 CC specific cells and tissues such as neuronal tissue, heart, liver,
 CC pancreas and adrenal gland. They are also useful for the construction of
 CC transgenic and knockout animals for studying SGT4 function in vivo and
 CC for the screening of SGT4 (ant)agonists in an animal model. Other more
 CC general uses include: as molecular weight markers on Southern gels; as
 CC chromosome markers or tags; as probes; for selecting and making
 CC oligomers for attachment to a gene chip; to raise anti-protein or
 CC anti-DNA antibodies or to elicit immune response. They are also
 CC also be used as nutritional sources or supplements such as in animal
 CC feed.
 XX
 SQ Sequence 1116 BP; 343 A; 224 C; 265 G; 284 T; 0 other;

Query Match 100.0%; Score 681; DB 22; Length 1116;
 Best Local Similarity 100.0%; Pred. No. 9.7e-198;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||
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QY      601 aagacctataatgaagaaccttaagaagaagaatctgttccagctataccaccaagctg 660
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Db      1096 tcttttagaccttaacttga 1116

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RESULT 3

AAH17218

ID AAH17218 standard; cDNA; 2056 BP.

AC AAH17218;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:16594.

KW Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EPI074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX

DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX

PS Claim 8; SEQ ID 16594; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dt primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX

SQ Sequence 2056 BP; 642 A; 394 C; 495 G; 525 T; 0 other;

Query Match 19.1%; Score 130.4; DB 22; Length 2056;
 Best Local Similarity 99.2%; Pred. No 1.5e-29;
 Matches 131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1291 gacataatggaagtgaaagcgatcgcaacatttgaataagaagatgaagcctat 1350
QY      610 attgaagaaccttaagaagaagaatctgttccagctataccaccaagaagtctttgagc 669
      |||
Db      1351 attgaagaaccttaagaagaagaatctgttccagctataccaccaagaagtctttgagc 1410
QY      670 cttaacttga 681
      |||
Db      1411 cttaacttga 1422

```

RESULT 4

AAFS8252

ID AAFS8252 standard; DNA; 936 BP.

AC AAFS8252;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D1835.

XX Electron-transfer group; ETM; mismatch; genotyping;

XX gene expression; ss.

XX

OS	Synthetic.
XX	
FN	WO200107665-A2.
XX	
PD	01-FEB-2001.
XX	
PF	26-JUL-2000; 2000WO-US0476.
XX	
PR	26-JUL-1999; 99US-0145695.
PR	17-MAR-2000; 2000US-0190259.
PA	(CLIN-) CLINICAL MICRO SENSORS INC,
XX	
PI	Umek RM;
XX	
DR	WPI; 2001-159728/16.
XX	
PT	Nucleic acids containing electron-transfer group, useful as labels in
PT	hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX	a single surface
XX	
PS	Example 6; Page 127; 159pp; English.
XX	
CC	The present invention relates to a composition comprising two nucleic
CC	acids each containing an electron-transfer group (ETM) having
CC	different redox potentials. The invention is used for electronic
CC	detection of nucleic acids, especially of substitutions (mismatches)
CC	and single-nucleotide polymorphisms, e.g. for genotyping,
CC	monitoring gene expression.
XX	
50	Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

[illegible][illegible]

RESULT 5
AAF58254

ID AAF58254 standard; DNA; 936 BP.

AC AAF58254;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D1875.

Electron-transfer group; ETM; mismatch; genotyping;

gene expression; ss.

OS Synthetic.

PN WO200107665-A2.
XX

PD 01-FEB-2001.
VY

PF 26-JUL-2000; 2000WO-US20476.
XY

PR	26-JUL-1999;	99US-0145695.
PR	17-MAR-2000.	2000US-0190259

XX
PA (CLTN-) CLINICAL MICRO SENSORS INCTimek RM:
XX
PT

XX WPT. 2001-159728/16

XX Nucleic acids containing electron-transfer group, useful as labels in DT

PT hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface -

Example 6: Page 127: 159nn: English
XX
PS

The present invention relates to a composition comprising two nucleic

CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic

CC detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms: a good method for genotyping.

CC monitoring gene expression.
XY

Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

Query Match 11 5% Score 78 6. DB 22. Length 936

Best Local Similarity 0.98; Pred. No. 6.3e-14;
Matches 6: Conservative 397; Mismatches 276; Indels 0: Gaps 0:

ov 1 atgaaattctaatctaccacaaataaaccaaatctcaaatcttccaaacaaataatcaattat 60

[illegible]

61 +tcaaaccaacatcaaatatctcaaacacattcctccaaagaa 120

[illegible]

```

001  +-----+-----+-----+-----+-----+-----+-----+-----+
101  +-----+-----+-----+-----+-----+-----+-----+-----+

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[illegible]

```

Db 175 wwwwwwwwwgwwwwwwwwwwwwwwwwwwwwwwwwwww 234
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Db 235 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 294
Qy 241 ttcttcagtgcccaactgtgtctcgcgattgcgaatttcagtggttgatcagc 300
Db 295 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 354
Qy 301 agcaataacctgacgcagcctgcgcgaagatagacagctagaagagctgcagagctt 360
Db 355 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 414
Qy 361 ctctgtataaaacaagttagacctctccctattccattcgttgtaacctgaagagctc 420
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Db 655 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 714
Qy 661 tctttagccttcaactt 679
Db 715 wwwwwwwwwwwwwwwwww 733

RESULT 6
AAFS8257
ID AAF58257 standard; DNA; 936 BP.
XX
AC AAF58257;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1954.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000HO-US20476.
XX
PR 26-JUL-1999; 990S-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
XX a single surface - e.g. for genotyping, allowing repeat analyses on
XX

```

```

PS Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
XX monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

```

```

Query Match 11.5%; Score 78.6; DB 22; Length 936;
Best Local Similarity 0.9%; Pred. No. 6.3e-14;
Matches 6; Conservative 397; Mismatches 276; Indels 0; Gaps 0;

```

```

Qy 1 atagaaattctgattgcacaaaacaaatctcacattccagcagaatcgtgt 60
Db 55 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 114
Qy 61 ttgaagacctgaagaacctcatgtgtttcaactatctgaagagcattcccgaa 120
Db 115 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 174
Qy 121 ttggagatttgaaatctagagagactgattgttctgaaatctagaattaatgag 180
Db 175 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 234
Qy 181 ctgccttgaatgaatgaatgaagcaagttacatttgatgatccagcaaaag 240
Db 235 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 294
Qy 241 ttcttcagtgcccaactgtgtctcgcgattgcgaatttcagtggttgatcagc 300
Db 295 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 354
Qy 301 agcaataacctgacgcagcctgcgcgaagatagacagctagaagagctgcagagctt 360
Db 355 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 414
Qy 361 ctctgtataaaacaagtgacacctccctccattccagctgaacctgaagaagctc 420
Db 415 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 474
Qy 421 actctgttagtcgtagtgaggacatttgtagagctcccaactgcctttagactca 480
Db 475 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 534
Qy 481 tccacaccttaaaatttgtaagcctatgagacaatcctatgataatgcccaatgtgaa 540
Db 535 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 594
Qy 541 gatggcaatgaataatgtgaagtgacgggacgcgaacatttgataagaagtattg 600
Db 595 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 654
Qy 601 aaagcctatagaaagccttaagaagaagaatctgttccagctataccacaaagt 660
Db 655 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 714
Qy 661 tctttagccttcaactt 679
Db 715 wwwwwwwwwwwwwwwwwwwww 733

RESULT 7
AAFS8259
ID AAF58259 standard; DNA; 936 BP.
XX
AC AAF58259;
XX
DT 24-APR-2001 (first entry)
XX

```

```
DE Oligonucleotide D2004.
XX
KM Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PS a single surface _
XX
PS Example 6; Page 128; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match      11.5%; Score 78.6; DB 22; Length 936;
Best Local Similarity 0.9%; Pred.No.6,3e-14;
Matches 6; Conservative 397; Mismatches 276; Indels 0; Gaps 0;

QY 1 atggaattctggatctgcacaaaccacaatctacatcttcagcgagaatcgttgt 60
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
55 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 114

OY 61 ttgaagaacctgaagaactcaatgttggttcaactatcgaagagcatccacaaa 120
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
115 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 174

OY 121 ttggagatttgaaatactagaagactgattgtctggaatctagaattaaggag 180
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
175 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 234

OY 181 ctgcccttgaattaagttaattgaagaagttacattttagatatctcagaacaag 240
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
235 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 294

OY 241 ttctccagtgcccacatctgtgtcctgagatcgtgaattgcaatgtgttatcacg 300
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
295 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 354

OY 301 agcaataaccctgaccgacctgcgcaagatalagacagctlagaggactgcagactlt 360
Db   : : : : : : : : : : : : : : : : | : : : : : : : : : :
355 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 414

OY 361 ctctctgatalaaaaaacagttgaacctacttccctatttccaatgctgaacctgaagactc 420
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
415 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 474

OY 421 actcgttagctgcgtcagtgaggagaccatttgttggagctcccaacgcaccttgtgtacca 480
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
475 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 534
```

```

Oy      481 tccacactttaaattgtgaagcctatgacaacctatctgtaataggccaagtga   540
Db       : : : ..... : : : : : ..... : : : |:: 594
        www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww
Oy      541 gatgcacgaataatgbagaagtgaacgggatcgccaacatttgataaagaattatg   600
        : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db       www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww
Oy      601 aaagcctatatgaagaccctaagaagaaggaaatcgtttcccagctatacaccaaatg   660
        : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db       www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.cwww.wwwww.wwwww.wwwww
Oy      661 tccttagcctcaacctt 679
        : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db       www.wwwww.wwwww.wwwww.wwwww 713

RESULT    8
AAF58262
ID AAF58262 standard; DNA; 936 BP.
AC
PC AAF58262;
XX
XX 24-APR-2001 (first entry)
DT
DE Oligonucleotide D2007.
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
OS Synthetic.
XX WO200107665-A2.
PN
PD 01-FEB-2001.
PP
PR 26-JUL-2000; 2000MO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000OUS-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
DR WPI: 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX
PS Example 6; Page 128; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
CX
CX SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match          11.5%; Score 78.6; DB 22; Length 936;
Best Local Similarity 0.9%, Pred. NO. 6.3e-14;
Matches     6; Conservative 397; Mismatches 276; Indels 0; Gaps 0;

Oy      1 atgaagaattcggatcgcgcaaanaaaccaatctcacatcttcagcagaatcgytgt 60
        :::::::::::::
Db       55 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww
        114
Oy      61 ttgaagaacctgaagaactcaatcygtygttcacactatcgaagagcatctccacgaa 120
```

[illegible]

XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX
PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETG) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
XX monitoring gene expression.
XX
50 Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match	11.5%;	Score 78.6;	DB 22;	Length 938;
Best Local Similarity	0.9%;	Pred. No. 6.3e-14;		
Matches	6;	Conservative 397;	Mismatches 276;	Indels 0;
				Gaps 0;

OY	1	atggaattctggagctgcgcaaaaacccaattccacttccagcaagaattggtt	60
Db	55	#####	114
OY	61	ttaagaacctgaagaagcaactatgttggtttcaactatctgaagacattctccagaa	120
Db	115	#####	174
OY	121	ttgggaattgtgaatactcagagagactgattgttctcggaactctgaattaatgag	180
Db	175	#####	234
OY	181	ctgcacctgaattaaatttgaagcaagttacatttgtatatactcagcaacaag	240
Db	235	#####	294
OY	241	tttccagttgccaatctgtctgcctcgagatgtcgaaatttcagtggttgatacagc	300
Db	295	#####	354
OY	301	agcaataacctgaccgcgcgcgaagatatagacagctagaggagctgcagactt	360
Db	355	#####	414
OY	361	ctcttgtataaacaagttgacctacttccctatctcatgtcgaaactgagaagctc	420
Db	415	#####	474
OY	421	aactctgttagctgcagtgggagcaatttgggtgagctcccaactgccttgyactca	480
Db	475	#####	534
OY	481	tccaaccttaaatattgtgaagccttatgacaatccattgataatgccaatgtaa	540
Db	535	#####	594
OY	541	gatggcaatgaataatgagaagtgaaacggatcgccaactttgataaagaattatg	600
Db	595	#####	654
OY	601	aagaccataattgaagacccttaagaagaagaatctgttccagctataccaccaagt	660
Db	655	#####	714
OY	661	tctttagcttcaactt 679	
Db	715	##### 733	
RESULT	10		
DD	AAAF58252/c		
DD	AAAF58252 standard: DNA: 936 BP.		

XX AAF58252;
AC
XX
XX 24-APR-2001 (first entry)
DT
XX
DE Oligonucleotide D1835.
KW
XX Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
XX
OS Synthetic.
CS
WN W0200107665-A2.
PN
XX
PD 01-FEB-2001.
PE
PF 26-JUL-2000; 200OWO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 200OUS-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI
PM Umeek RM;
PS
DR WP1; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PP a single surface -
XX
PS Example 6; Page 127; 159pp; English.

The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.

Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

	Query Match	11.4%	Score 77.4	DB 22	Length 936	
	Best Local Similarity	0.9%	Pred. No. 1.5e-13			
	Matches	6	Conservative 390	Mismatches 17	Indels 0	Gaps 0
QY	1 atgagaattctgacatctgcacaataaccacatctcacatcttcagcagcaaatcggtt	60				
Db	775 WWWWWWWW.....	716				
QY	61 ttgaagaacctgaagaactcaaagtgggttcaactatcgaagagcatccccaaga	120				
Db	715 WWWWWWWW.....G.....	656				
QY	121 ttggagagtttgaaactagagagactgtagtttctcggaalctgtaatatgag	180				
Db	655 WWWWWWWW.....	596				
QY	181 ctgcccttgaattgaatgaattgaagcaagtacatttgtatatactcagcaacaag	240				
Db	595 WNNCWWWWWW.....	536				
QY	241 ttttcagttgccacatctgtgctctgcggaatgcgaatttcgaattgctgttgataccagc	300				
Db	535 WNNWWWWWWWW.....N.....	476				
QY	301 agcaataactcyaacgcacctgcgcaagatalagaacaggctagagagctgcagac	360				
Db	475 WNNWWWWWWWW.....	416				
QY	361 cttctgtataaaaacaagttgacctacattccctatccatctcgaatgaagaagctc	420				

[illegible]

Query Match	Similarity	Score	DB	Length	936;
Best Local	6;	Conservative	390;	Mismatches	271;
Indels	0;	Gaps	0;		

Query Match 11.4%; Score 77.4; DB 22; Length 936;
Best Local Similarity 0.9%; Pred. No. 1.5e-13;
Matches 6; Conservative 390; Mismatches 271; Indels 0; Gaps 0;

```
QY 1 atgagaattcgtgctgcgaataaaccaatctcacatcttcacagagaatcggtgt 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 775 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 716
QY 61 ttgaagaacctgaagaactcaatggtgttcaactatctgaagaagatccctcgaa 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 715 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 656
QY 121 ttggagagatgtgaataactgaagagactggtcttctgaatactagaatgag 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 655 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 596
QY 181 ctgccttgaatgaatgaatgaagaagttacattgtgatctcagaacaag 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 595 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 536
QY 241 ttcccggtgcccaatctgtctcgcgagtcgcgaattgtcggtgttgatacagc 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 535 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 476
QY 301 agcaataacctgaccgcctgcgcaagataagacaggtagagagctgcagagctt 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 416
QY 361 ctctgtataaacaagtgcacttccctcattccatcgcgtgaactgaagaagctc 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 415 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 356
QY 421 actctgttagtcgcactggtgggacatttgggtgagctcccaactgccttctgactca 480
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 355 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 296
QY 481 tccacaccttaaatlttgtagcttgtagacactctatgtgataatgccaatgtaa 540
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 236
QY 541 gatgcaatgaataatgtaagtgaaacggaatcgccaactttgataaagaagtatg 600
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 176
QY 601 aaagcctatatgaagaccttaagaagaagaatctgttccagctataccacaagtg 660
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 116
QY 661 tcttlla 667
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 109
```

RESULT 15
AAF58255/c
ID AAF58255 standard; DNA; 938 BP.

XX AAF58255;

XX 24-APR-2001 (first entry)

DE Oligonucleotide D1876.

XX Electron-transfer group; ETM; mismatch; genotyping;

KW gene expression; ss.

XX Synthetic.

PN W0200107665-A2.

XX 01-FEB-2001.

PF 26-JUL-2000; 2000WO-US20476.
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.

XX (CLIN-) CLINICAL MICRO SENSORS INC.

PI Unek RM;

XX WPI; 2001-159728/16.

XX Nucleic acids containing electron-transfer group, useful as labels in

PT hybridization assays, e.g. for genotyping, allowing repeat analyses on

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CC and single-nucleotide polymorphisms, e.g. for genotyping,

CC monitoring gene expression.

XX Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 11.4%; Score 77.4; DB 22; Length 938;

Best Local Similarity 0.9%; Pred. No. 1.5e-13;

Matches 6; Conservative 390; Mismatches 271; Indels 0; Gaps 0;

```
QY 1 atgagaattcgtgctgcgaataaaccaatctcacatcttcacagagaatcggtgt 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 775 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 716
QY 61 ttgaagaacctgaagaactcaatggtgttcaactatctgaagaagatccctcgaa 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 715 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 656
QY 121 ttggagagatgtgaataactgaagagactggtcttctgaatactagaatgag 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 655 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 596
QY 181 ctgccttgaatgaatgaatgaagaagttacattgtgatctcagaacaag 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 595 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 536
QY 241 ttcccggtgcccaatctgtctcgcgagtcgcgaattgtcggtgttgatacagc 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 535 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 476
QY 301 agcaataacctgaccgcctgcgcaagataagacaggtagagagctgcagagctt 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 416
QY 361 ctctgtataaacaagtgcacttccctcattccatcgcgtgaactgaagaagctc 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 415 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 356
QY 421 actctgttagtcgcactggtgggacatttgggtgagctcccaactgccttctgactca 480
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 355 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 296
QY 481 tccacaccttaaatlttgtagcttgtagacactctatgtgataatgccaatgtaa 540
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 236
QY 541 gatgcaatgaataatgtaagtgaaacggaatcgccaactttgataaagaagtatg 600
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 176
QY 601 aaagcctatatgaagaccttaagaagaagaatctgttccagctataccacaagtg 660
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Db 175 WWWXX 116
QY 661 tottta 667
: : : : :
Db 115 WWWXXXX 109

Search completed: February 26, 2002, 10:47:46
Job time: 10583 sec